



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/009,445B  
Source: IFW16  
Date Processed by STIC: 10-12-04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER  
VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - cPAVE)

2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450

3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):

U.S. Patent and Trademark Office, 220 20<sup>th</sup> Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two Lobby,  
Room 1B03, Arlington, VA 22202

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER:

10/009,445 B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics  
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino Numbering The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) \_\_\_\_\_ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences (OLD RULES) Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO: X (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS (Do not insert any subheadings under this heading!)  
(ii) SEQUENCE DESCRIPTION SEQ ID NO: X (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES" response to include the skipped sequences.
- 8 Skipped Sequences (NEW RULES) Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence:  
<210> sequence id number  
<400> sequence id number  
000
- 9 Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213> Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence.
- 11 Use of <220> Sequence(s) \_\_\_\_\_ missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See: "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid.

(pg. 6-7)

Does Not Comply  
Corrected Diskette Needed

(pg. 3, 6)

## RAW SEQUENCE LISTING

DATE: 10/12/2004

PATENT APPLICATION: US/10/009,445B

TIME: 11:51:41

Input Set : D:\14094-20009.00 - Substitute Seqlist.txt

Output Set: N:\CRF4\10122004\J009445B.raw

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65 Cys Pro Asp Lys Asn Gln Thr Met Gln Asn Asn Ser Ser Thr Met Thr
66 1 5 10 15
68 gaa gtt aac act aca gtg ttt gta cag atg ggt aaa aag gct ctg ctc 258
69 Glu Val Asn Thr Thr Val Phe Val Gln Met Gly Lys Lys Ala Leu Leu
70 20 25 30
72 tgc tgc cct tct att tca ctg aca aaa gta ata tta ata aca tgg aca 306
73 Cys Cys Pro Ser Ile Ser Leu Thr Lys Val Ile Leu Ile Thr Trp Thr
74 35 40 45
76 ata acc ctc aga gga cag cct tcc tgc ata ata tcc tac aaa gca gac 354
77 Ile Thr Leu Arg Gly Gln Pro Ser Cys Ile Ile Ser Tyr Lys Ala Asp
78 50 55 60
80 aca agg gag acc cat gaa agc aac tgc tgc gac aga agc atc acc tgg 402
81 Thr Arg Glu Thr His Glu Ser Asn Cys Ser Asp Arg Ser Ile Thr Trp
82 65 70 75 80
84 gcc tcc aca cct gac ctc gct cct gac ctt cag atc agt gca gtg gcc 450
85 Ala Ser Thr Pro Asp Leu Ala Pro Asp Leu Gln Ile Ser Ala Val Ala
86 85 90 95
88 ctc cag cat gaa ggg cgt tac tca tgt gat ata gca gta cct gac ggg 498
89 Leu Gln His Glu Gly Arg Tyr Ser Cys Asp Ile Ala Val Pro Asp Gly
90 100 105 110
92 aat ttc caa aac atc tat gac ctc caa gtg ctg gtg ccc cct gaa gta 546
93 Asn Phe Gln Asn Ile Tyr Asp Leu Gln Val Leu Val Pro Pro Glu Val
94 115 120 125
96 acc cac ttt cca ggg gaa aat aga act gca gtt tgt gag gcg att gca 594
97 Thr His Phe Pro Gly Glu Asn Arg Thr Ala Val Cys Glu Ala Ile Ala
98 130 135 140
100 ggc aaa cct gct gcg cag atc tct tgg acg cca gat ggg gat tgt gtc 642
101 Gly Lys Pro Ala Ala Gln Ile Ser Trp Thr Pro Asp Gly Asp Cys Val
102 145 150 155 160
104 gct aag aat gaa tca cac agc aat ggc acc gtg act gtc cgg agc aca 690
105 Ala Lys Asn Glu Ser His Ser Asn Gly Thr Val Thr Val Arg Ser Thr
106 165 170 175
108 tgc cac tgg gag cag agc cac gtg tct gtc gtg ttc tgt gtt gtc tct 738
109 Cys His Trp Glu Gln Ser His Val Ser Val Val Phe Cys Val Val Ser
110 180 185 190
112 cac ttg aca act ggt aac cag tct ctg tct ata gaa ctg ggt aga ggg 786
113 His Leu Thr Thr Gly Asn Gln Ser Leu Ser Ile Glu Leu Gly Arg Gly
114 195 200 205
116 ggt gac caa tta tta gga tca tac att caa tac atc atc cca tct att 834
117 Gly Asp Gln Leu Leu Gly Ser Tyr Ile Gln Tyr Ile Ile Pro Ser Ile
118 210 215 220
120 att att ttg atc atc ata gga tgc att tgt ctt ttg aaa atc agt ggc 882
121 Ile Ile Leu Ile Ile Ile Gly Cys Ile Cys Leu Leu Lys Ile Ser Gly
122 225 230 235 240
124 tgc aga aaa tgt aaa ttg cca aaa tgc gga gct act cca gat att gag 930
125 Cys Arg Lys Cys Lys Leu Pro Lys Ser Gly Ala Thr Pro Asp Ile Glu
126 245 250 255
128 gag gat gaa atg cag ccg tat gct agc tac aca gag aag agc aat cca 978
129 Glu Asp Glu Met Gln Pro Tyr Ala Ser Tyr Thr Glu Lys Ser Asn Pro

```

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Input Set : D:\14094-20009.00 - Substitute Seqlist.txt

Output Set: N:\CRF4\10122004\J009445B.raw

130 260 265 270  
 132 ctc tat gat act gtg acc acg acg gag gca cac cca gcg tca caa ggc 1026  
 133 Leu Tyr Asp Thr Val Thr Thr Thr Glu Ala His Pro Ala Ser Gln Gly  
 134 275 280 285  
 136 aaa gtc aat ggc aca gac tgt ctt act ttg tca gcc atg gga atc 1071  
 137 Lys Val Asn Gly Thr Asp Cys Leu Thr Leu Ser Ala Met Gly Ile  
 138 290 295 300  
 140 tagaaccaag gaaaagaagt caagagacat cataattact gcttttcttt ctttaaactt 1131  
 142 ctccaatgga gggaaattag ctcttctgaa gttcttagaa agcacaaatg ttctaattga 1191  
 144 tttgccttta agttcttcta tcattggaag tttggaatct ttgctgctac ctgttaattc 1251  
 146 taggaagaac tgatttaatt attacaaaga aagcacattg ttatggtaaa atatcaaatt 1311  
 148 gtgcaataca atgatgaaaa ctgagtttcc tcaagaaata actgcagaag gaacaatcat 1371  
 150 tactaaagca tttcatgtga gttcttccaa aaaagaaaat ccctgtgtat acgacatgat 1431  
 152 tatggtatgt gtgtgccttt atatgtttgt ttacaaatgt gtatatatgc acacatctga 1491  
 154 ttatcaagac atctctgtca aaaactcact ggcgttcag atttatgaaa gctaataaag 1551  
 156 tgagtattgg agatgttttt ata 1574  
 159 <210> SEQ ID NO: 2  
 160 <211> LENGTH: 327  
 161 <212> TYPE: PRT  
 162 <213> ORGANISM: Unknown  
 W--> 164 <220> FEATURE:  
 W--> 164 <223> OTHER INFORMATION:  
 W--> 164 <400> 2  
 165 Met Leu Cys Phe Trp Arg Thr Ser His Val Ala Val Leu Leu Ile Trp  
 166 -20 -15 -10  
 168 Gly Val Phe Ala Ala Glu Ser Ser Cys Pro Asp Lys Asn Gln Thr Met  
 169 -5 -1 1 5  
 171 Gln Asn Asn Ser Ser Thr Met Thr Glu Val Asn Thr Thr Val Phe Val  
 172 10 15 20  
 174 Gln Met Gly Lys Lys Ala Leu Leu Cys Cys Pro Ser Ile Ser Leu Thr  
 175 25 30 35 40  
 177 Lys Val Ile Leu Ile Thr Trp Thr Ile Thr Leu Arg Gly Gln Pro Ser  
 178 45 50 55  
 180 Cys Ile Ile Ser Tyr Lys Ala Asp Thr Arg Glu Thr His Glu Ser Asn  
 181 60 65 70  
 183 Cys Ser Asp Arg Ser Ile Thr Trp Ala Ser Thr Pro Asp Leu Ala Pro  
 184 75 80 85  
 187 Asp Leu Gln Ile Ser Ala Val Ala Leu Gln His Glu Gly Arg Tyr Ser  
 188 90 95 100  
 190 Cys Asp Ile Ala Val Pro Asp Gly Asn Phe Gln Asn Ile Tyr Asp Leu  
 191 105 110 115 120  
 193 Gln Val Leu Val Pro Pro Glu Val Thr His Phe Pro Gly Glu Asn Arg  
 194 125 130 135  
 196 Thr Ala Val Cys Glu Ala Ile Ala Gly Lys Pro Ala Ala Gln Ile Ser  
 197 140 145 150  
 199 Trp Thr Pro Asp Gly Asp Cys Val Ala Lys Asn Glu Ser His Ser Asn  
 200 155 160 165  
 202 Gly Thr Val Thr Val Arg Ser Thr Cys His Trp Glu Gln Ser His Val  
 203 170 175 180

PLS see error explanation on page 8. ↓

PLS insert, whenever <213> response is artificial Unknown or Genus/Species.

↑  
 The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

## RAW SEQUENCE LISTING

DATE: 10/12/2004

PATENT APPLICATION: US/10/009,445B

TIME: 11:51:41

Input Set : D:\14094-20009.00 - Substitute Seqlist.txt

Output Set: N:\CRF4\10122004\J009445B.raw

```

205 Ser Val Val Phe Cys Val Val Ser His Leu Thr Thr Gly Asn Gln Ser
206 185                      190                      195                      200
208 Leu Ser Ile Glu Leu Gly Arg Gly Gly Asp Gln Leu Leu Gly Ser Tyr
209                      205                      210                      215
211 Ile Gln Tyr Ile Ile Pro Ser Ile Ile Ile Leu Ile Ile Ile Gly Cys
212                      220                      225                      230
214 Ile Cys Leu Leu Lys Ile Ser Gly Cys Arg Lys Cys Lys Leu Pro Lys
215                      235                      240                      245
217 Ser Gly Ala Thr Pro Asp Ile Glu Glu Asp Glu Met Gln Pro Tyr Ala
218                      250                      255                      260
220 Ser Tyr Thr Glu Lys Ser Asn Pro Leu Tyr Asp Thr Val Thr Thr Thr
221 265                      270                      275                      280
223 Glu Ala His Pro Ala Ser Gln Gly Lys Val Asn Gly Thr Asp Cys Leu
224                      285                      290                      295
226 Thr Leu Ser Ala Met Gly Ile
227                      300
230 <210> SEQ ID NO: 3
231 <211> LENGTH: 1604
232 <212> TYPE: DNA
233 <213> ORGANISM: Unknown
235 <220> FEATURE:
236 <223> OTHER INFORMATION: Description of Unknown Organism:primate; surmised
237     homo sapiens
239 <220> FEATURE:
240 <221> NAME/KEY: CDS
241 <222> LOCATION: (217)..(1101)
243 <220> FEATURE:
244 <221> NAME/KEY: mat_peptide
245 <222> LOCATION: (295)..(1101)
247 <400> SEQUENCE: 3
248 cagagaaaag cttctgttcg tccaagttac taaccaggct aaaccacata gacgtgaagg 60
250 aaggggctag aaggaaggga gtgccccact gttgatggg taagaggatc ctgtactgag 120
252 aagttgacca gagagggtct caccatgcgc acagttcctt ctgtaccagt gtggaggaaa 180
254 agtactgagt gaagggcaga aaaagagaaa acagaa atg ctc tgc cct tgg aga 234
255                      Met Leu Cys Pro Trp Arg
256                      -25
258 act gct aac cta ggg cta ctg ttg att ttg act atc ttc tta gtg gcc 282
259 Thr Ala Asn Leu Gly Leu Leu Leu Ile Leu Thr Ile Phe Leu Val Ala
260 -20                      -15                      -10                      -5
262 gaa gcg gag ggt gct gct caa cca aac aac tca tta atg ctg caa act 330
263 Glu Ala Glu Gly Ala Ala Gln Pro Asn Asn Ser Leu Met Leu Gln Thr
264                      -1    1                      5                      10
266 agc aag gag aat cat gct tta gct tca agc agt tta tgt atg gat gaa 378
267 Ser Lys Glu Asn His Ala Leu Ala Ser Ser Ser Leu Cys Met Asp Glu
268                      15                      20                      25
270 aaa cag att aca cag aac tac tcg aaa gta ctc gca gaa gtt aac act 426
271 Lys Gln Ile Thr Gln Asn Tyr Ser Lys Val Leu Ala Glu Val Asn Thr
272                      30                      35                      40
274 tca tgg cct gta aag atg gct aca aat gct gtg ctt tgt tgc cct cct 474

```

## RAW SEQUENCE LISTING

DATE: 10/12/2004

PATENT APPLICATION: US/10/009,445B

TIME: 11:51:41

Input Set : D:\14094-20009.00 - Substitute Seqlist.txt

Output Set: N:\CRF4\10122004\J009445B.raw

```

275 Ser Trp Pro Val Lys Met Ala Thr Asn Ala Val Leu Cys Cys Pro Pro
276 45 50 55 60
278 atc gca tta aga aat ttg atc ata ata aca tgg gaa ata atc ctg aga 522
279 Ile Ala Leu Arg Asn Leu Ile Ile Ile Thr Trp Glu Ile Ile Leu Arg
280 65 70 75
282 ggc cag cct tcc tgc aca aaa gcc tac aag aaa gaa aca aat gag acc 570
283 Gly Gln Pro Ser Cys Thr Lys Ala Tyr Lys Lys Glu Thr Asn Glu Thr
284 80 85 90
286 aag gaa acc aac tgt act gat gag aga ata acc tgg gtc tcc aga cct 618
287 Lys Glu Thr Asn Cys Thr Asp Glu Arg Ile Thr Trp Val Ser Arg Pro
288 95 100 105
290 gat cag aat tcg gac ctt cag att cgt acc gtg gcc atc act cat gac 666
291 Asp Gln Asn Ser Asp Leu Gln Ile Arg Thr Val Ala Ile Thr His Asp
292 110 115 120
294 ggg tat tac aga tgc ata atg gta aca cct gat ggg aat ttc cat cgt 714
295 Gly Tyr Tyr Arg Cys Ile Met Val Thr Pro Asp Gly Asn Phe His Arg
296 125 130 135 140
298 gga tat cac ctc caa gtg tta gtt aca cct gaa gtg acc ctg ttt caa 762
299 Gly Tyr His Leu Gln Val Leu Val Thr Pro Glu Val Thr Leu Phe Gln
300 145 150 155
302 aac agg aat aga act gca gta tgc aag gca gtt gca ggg aag cca gct 810
303 Asn Arg Asn Arg Thr Ala Val Cys Lys Ala Val Ala Gly Lys Pro Ala
304 160 165 170
306 gcg cat atc tcc tgg atc cca gag ggc gat tgt gcc act aag caa gaa 858
307 Ala His Ile Ser Trp Ile Pro Glu Gly Asp Cys Ala Thr Lys Gln Glu
308 175 180 185
310 tac tgg agc aat ggc aca gtg act gtt aag agt aca tgc cac tgg gag 906
311 Tyr Trp Ser Asn Gly Thr Val Thr Val Lys Ser Thr Cys His Trp Glu
312 190 195 200
314 gtc cac aat gtg tct acc gtg acc tgc cac gtc tcc cat ttg act ggc 954
315 Val His Asn Val Ser Thr Val Thr Cys His Val Ser His Leu Thr Gly
316 205 210 215 220
318 aac aag agt ctg tac ata gag cta ctt cct gtt cca ggt gcc aaa aaa 1002
319 Asn Lys Ser Leu Tyr Ile Glu Leu Leu Pro Val Pro Gly Ala Lys Lys
320 225 230 235
322 atc agc aaa att ata tat tcc ata tat cat cct tac tat tat tat tta 1050
323 Ile Ser Lys Ile Ile Tyr Ser Ile Tyr His Pro Tyr Tyr Tyr Tyr Leu
324 240 245 250
326 gac cat cgt ggg att cat ttg gtt gtt gaa agt caa tgg ctg cag aaa 1098
327 Asp His Arg Gly Ile His Leu Val Val Glu Ser Gln Trp Leu Gln Lys
328 255 260 265
330 ata taaattgaat aaaacagaat ctactccagt tggtgaggag gatgaaatgc 1151
331 Ile
333 agccctatgc cagctacaca gagaagaaca atcctctcta tgatactaca aacaagggtga 1211
335 aggcattctga ggcattacaa agtgaagttg acacagacct ccatacttta taagttgttg 1271
337 gactctagta ccaagaaaca acaacaaacg agatacatta taattactgt ctgattttct 1331
339 tacagttcta gaatgaagac ttatatggaa attaggtttt ccaaggttct tagaagacat 1391
341 tttaatggat tctcattcat acccttgat aattggaatt tttgattctt agctgctacc 1451
343 agctagttct ctgaagaact gatgttatta caaagaaaat acatgcccac gaccaaatat 1511

```

<210> 21  
<211> 1044

<212> DNA

<213> reverse translation

<220>

<221> misc\_feature

<222> (1)..(1044)

<223> n may be a, c, g, or t

<400> 21

Invalid  
Response

Mandatory, <213>

Responses has to be  
either artificial/  
Unknown or Genus/  
Species. PLS see  
item # 10 on  
error summary  
Sheet.

The type of errors shown exist throughout  
the Sequence Listing. Please check subsequent  
sequences for similar errors.



RAW SEQUENCE LISTING ERROR SUMMARY      DATE: 10/12/2004  
PATENT APPLICATION: US/10/009,445B      TIME: 11:51:42

Input Set : D:\14094-20009.00 - Substitute Seqlist.txt  
Output Set: N:\CRF4\10122004\J009445B.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:13; N Pos. 6,18,21,24,30,33,36,39,42,51,54,60,63,69,72,78,93,108,111  
Seq#:13; N Pos. 114,120,126,132,135,138,144,153,162,165,168,177,180,186,189  
Seq#:13; N Pos. 192,198,204,210,216,222,225,228,231,237,240,252,261,267,270  
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Seq#:13; N Pos. 777,780,789,792,798,810,813,819,822,825,828,831,858,864,867  
Seq#:13; N Pos. 873,882,888,891,900,903,906,909,912,918,924,927,930,936,942  
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Seq#:14; N Pos. 474,477,480,486,498,501,510,516,519,522,525,528,534,537,540  
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Seq#:14; N Pos. 630,633,651,657,660,663,666,669,675,678,693,702,705,708,711  
Seq#:14; N Pos. 714,723,726,732,735,738,747,750,762,765,768,771,774,777,780  
Seq#:14; N Pos. 792,807,819,834,843,846,855,858,861,867,876  
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Seq#:16; N Pos. 234,240,243,246,249,261,267,276,279,282,288,291,300,309,312  
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Seq#:16; N Pos. 396,399,408,411,414,423,426,429,432,438,441,444,453,462,468  
Seq#:16; N Pos. 471,477,480,483,501,507,510,513,516,519,525,528,534,543,552  
Seq#:16; N Pos. 555,558,561,570,573,579,582,585,594,597,600,603,609,615,618  
Seq#:16; N Pos. 621,624,627,630,633,636,639,642,645,648,651,654,663,669,675  
Seq#:16; N Pos. 678,681,687,690,696,699,702,705,708,714,726,738,741,747,750  
Seq#:17; N Pos. 3,6,12,15,27,36,42,51,60,66,69,72,81,87,90,93,96,108,114

RAW SEQUENCE LISTING ERROR SUMMARY      DATE: 10/12/2004  
PATENT APPLICATION: US/10/009,445B      TIME: 11:51:42

Input Set : D:\14094-20009.00 - Substitute Seqlist.txt  
Output Set: N:\CRF4\10122004\J009445B.raw

Seq#:17; N Pos. 123,126,129,132,135,147,156,168,171,174,180,195,204,210,213  
Seq#:17; N Pos. 216,219,222,228,231,240,243,252,255,258,261,270,276,279,285  
Seq#:17; N Pos. 288,291,300,306,309,315,324,327,333,339,345,351,354,357,360  
Seq#:17; N Pos. 363,366,369,372,396,399,402,405,408,417,420,426,429,432,441  
Seq#:17; N Pos. 444,447,456,459,462,465,468,471,474,477,480,483,486,489,492  
Seq#:17; N Pos. 495,501,507,516,519,522,525,534,537,543,546,552,567,573,576  
Seq#:17; N Pos. 579,582

Use of <220> Feature(NEW RULES): *Error Explanation: 2*  
Sequence(s) are missing the <220> Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence"  
or "Unknown". Please explain source of genetic material in <220> to <223>  
section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32)  
(Sec.1.823 of new Rules)

Seq#:2,4,6,8,10,12,20,23

## VERIFICATION SUMMARY

DATE: 10/12/2004

PATENT APPLICATION: US/10/009,445B

TIME: 11:51:42

Input Set : D:\14094-20009.00 - Substitute Seqlist.txt

Output Set: N:\CRF4\10122004\J009445B.raw

L:164 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:2, <213>  
ORGANISM:Unknown  
L:164 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:2, <213>  
ORGANISM:Unknown  
L:164 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:164  
L:355 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:4, <213>  
ORGANISM:Unknown  
L:355 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:4, <213>  
ORGANISM:Unknown  
L:355 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:355  
L:541 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:6, <213>  
ORGANISM:Unknown  
L:541 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:6, <213>  
ORGANISM:Unknown  
L:541 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:541  
L:699 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:8, <213>  
ORGANISM:Unknown  
L:699 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:8, <213>  
ORGANISM:Unknown  
L:699 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8,Line#:699  
L:836 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:10, <213>  
ORGANISM:Unknown  
L:836 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:10, <213>  
ORGANISM:Unknown  
L:836 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:10,Line#:836  
L:992 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:12, <213>  
ORGANISM:Unknown  
L:992 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:12, <213>  
ORGANISM:Unknown  
L:992 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:12,Line#:992  
L:1059 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0  
M:341 Repeated in SeqNo=13  
L:1105 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0  
M:341 Repeated in SeqNo=14  
L:1147 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0  
M:341 Repeated in SeqNo=15  
L:1193 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0  
M:341 Repeated in SeqNo=16  
L:1231 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0  
M:341 Repeated in SeqNo=17  
L:1263 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0  
M:341 Repeated in SeqNo=18  
L:1405 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:20, <213>  
ORGANISM:Unknown  
L:1405 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:20, <213>  
ORGANISM:Unknown  
L:1405 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:20,Line#:1405  
L:1484 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:0  
M:341 Repeated in SeqNo=21  
L:1614 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:23, <213>  
ORGANISM:Unknown  
L:1614 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:23, <213>  
ORGANISM:Unknown

L:1614 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:23,Line#:1614  
L:1678 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:0  
M:341 Repeated in SeqNo=24